

UNBIASED MULTIPLE-SUBJECT ALIGNMENT OF LEFT VENTRICLES

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ABSTRACT

Image based quantitative stratification of the left ventricular (LV) pathology helps in understanding the structure-function symbiosis of the heart. However, this requires unbiased, referenceless multi-subject LV alignment that accounts for the physioanatomic variations associated with the pathology. This paper achieves this hitherto elusive alignment by adopting the conventional risk stratification strategies routinely followed by clinicians. The individual LV shape models are **independently** reoriented to an "*attitudinally consistent orientation*" that captures the physioanatomic and pathologic variations of the LV morphology. The proposed algorithm is computationally efficient and provides an efficient framework for constructing pathology stratified cardiac atlas.

Index Terms— Cardiac atlas, stratification, *attitudinally consistent orientation*, medial surface, dominant prong.

1. INTRODUCTION

Cardiovascular diseases have an equal opportunity presence accounting for thirty-three percent of annual worldwide deaths. Image based quantitation of the pathology associated morphologic alterations and personalization of this knowledge to the patient specific multidimensional data helps in assessing the patient's cardiac wellness. Clinicians have acquired the skills to perform such stratification mentally. However, automating this routine manual process requires a machine-learning step that involves collating data across multiple subjects into a statistical atlas to capture the pathology-specific morphology variations.

The atlas construction is usually accomplished via an image alignment process that establishes pair wise correspondence between two datasets and subsequently stitches multiple such correspondences to establish a joint homology. Such approaches suffer from the biased choice of a reference dataset to which others are aligned. To overcome this discrepancy, a number of unbiased, simultaneous registration schemes have been proposed [1-3]. These schemes align the multiple subjects to a common coordinate system by determining the most consistent alignment of the joint data. Though technically elegant, these techniques do not adhere to the clinician friendly "*attitudinally consistent*

orientation" [4] and require the simultaneous treatment of all the datasets under investigation.

This paper describes a technique that draws upon the clinically established protocol [5,6] of minimizing variations by reorienting the LV such that physioanatomic and pathological influences are well characterized. The approach is motivated from the following clinically exploited facts of the heart: (a) the heart's pose as deduced from the principal orientation of the LV serves as a unifying reference frame across different subjects [7]; (b) the motion of the LV through the cardiac cycle can be separated into global translation, longitudinal and circumferential shortening or elongation [8]; (c) acquisition during the diastolic phase of the cardiac cycle provides a dataset with least motion artifacts [9]; and (d) quantitative morphology along the short-axis of the LV facilitates robust pathology stratification [10]. By cascading the above-mentioned facts into an algorithmic pipeline, the proposed approach reorients the shape models of the individual LVs **independently** into a consistent physioanatomic space, and in the process maximizes the joint similarities between the datasets. The proposed algorithm could help in constructing unbiased pathology stratified cardiac atlases.

2. MATERIALS AND METHODS

2.1. Data Acquisition

The datasets for this study were selected from the cardiac CT scans acquired at Narayana Hrudhayalaya, Bangalore, India using a 64-slice Lightspeed VCT (GE Healthcare) MDCT scanner. Acquisitions from patients with atypical chest pain, those requiring corrective surgery and potentially normal subjects who participated in the mandatory executive screening were included in this study. In accordance with the clinical protocol, the heart rate of the subjects was, where required, ionotropically controlled using beta-blockers. Personalized BMI-adjusted tube current and retrospective ECG gating was used during the acquisition. High temporal resolution images were obtained by reconstructing the data with partial scan reconstruction at 75% interval in R-R ECG cycle. As shown in Figure 1, this interval corresponds to the *diastolic* phase of the cardiac cycle; in this interval there is minimal blood flow into the LV and consequently, the LV is very nearly static with negligible differential apical-basal motion. By controlling the heart rate during acquisition, and

reconstructing the LV at the diastolic interval, the physiological variations associated with a given pathology is minimized.

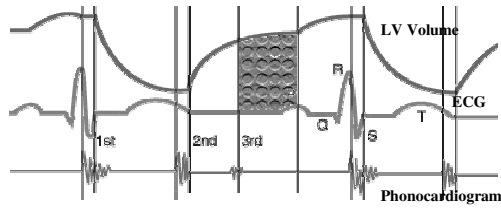


Figure 1. Acquiring the data during the diastolic phase (shaded area) of the cardiac cycle reduces the physiology induced anatomical variations for the given pathology.

2.2. Construction of LV Shape Model

The LV shape model was built using an interactive segmentation tool available in the GE Healthcare Advantage Windows (AW) workstation. In consultation with expert radiologists, trained 3D technicians sparsely segmented the key LV sections using the border tracing tool; the sparse segmentations were populated using a shape propagation technique. Topology preserving smoothing based on curvature flow was applied to the populated shape model to account for the out-of-plane edge incoherency.

2.3 Generation of Attitudinally Consistent Orientation

To characterize the pathology related variations in LV morphology, it is essential to minimize the confounding effects of the baseline physiological perturbations arising primarily from the incorrect phase selection during the reconstruction process. As mentioned before, the motion of the LV through the cardiac cycle can be distinctly separated into global translation, longitudinal and circumferential shortening or elongation [8]. By **independently** translating the individual LV shape models to a common origin and reorienting them so that their orthogonal axes correspond to the directions of longitudinal and circumferential scaling, the respective models can be aligned to the clinically recognized “*attitudinally consistent orientation*”. Grouping the LVs in this consistent position facilitates the quantification of the physioanatomic and pathologic variations in the morphology.

The global translation is synchronized by computing the centroids of the individual LV and shifting them to a common origin. The following sections describe the steps involved in establishing consistent orientation.

2.3.1 Pose Estimation

The longitudinal axis of the LV spans across the apex and the base; this axis corresponds to the most dominant orientation (pose) of the LV shape model. The dominant orientation is captured from the shape's second order moment via the Principal Component Analysis (PCA).

Aligning the dominant orientation of the individual models **independently** to a “common axis” (in this study x- axis was used as the common axis) establishes a consistent longitudinal framework across all the models. Figure 2 illustrates the longitudinal alignment.

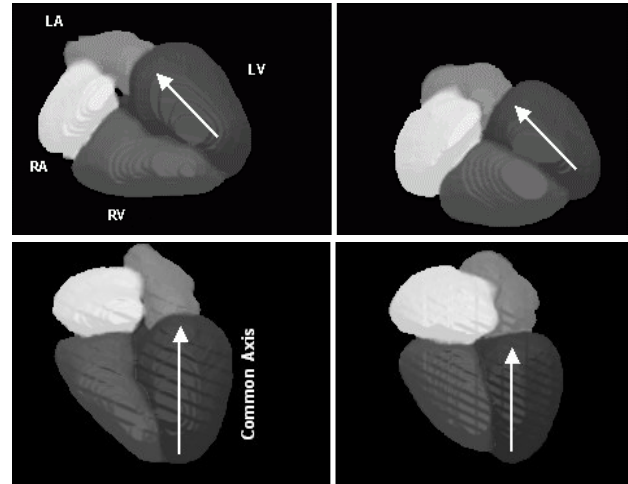


Figure 2. Consistent inter-subject LV pose (bottom row) is achieved by independently aligning the principal Eigen vectors of the individual LV shape models (top row) to a common axis.

2.3.2 In-plane Alignment

As mentioned previously, quantitative morphology along the short-axis of the LV facilitates robust pathology stratification. While the PCA based alignment provides a referenceless, unbiased longitudinal orientation consistency across the LV shape model, it does not guarantee a consistent in-plane orientation. Correcting for this inconsistency in an independent, unbiased and referenceless manner is a challenge and requires exploiting the salient features of the cardiac architecture.

Within the LV, an organ in a state of perpetual flux, the aortic vestibule and the immediate vicinity of the mitral valve are stationary across the cardiac cycle [7]. Identifying and suitably orienting key landmarks within this region could provide a consistent in-plane orientation and hence better overall alignment. Since the data is acquired during the diastolic *diastolic* phase, landmarks around the then open mitral valve will be inaccurate; a salient region within the aortic vestibule preferably proximal to the closed aortic valve will be a landmark of choice. Such a landmark could be identified efficiently by traversing through the medial surface (MS) of the LV shape model. The following section describes the steps to identify the landmark on the aortic valve.

2.3.2.1 MS of the LV

A number of efficient algorithms exist for constructing the MS of a given shape. In this study, the Parameter controlled skeletonization proposed in [11] was used. Briefly, the method uses the fact that any point on the MS should be the

local maxima in the distance transform space. The local maxima locations greater than the mean neighborhood distance is identified as a candidate location in MS. Figure 3 shows the MS generated by this method for a representative LV.

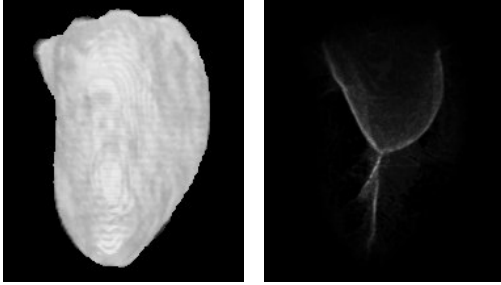


Figure 3. Parameter-skeleton based MS (right) of a LV shape model (left)

2.3.2.2 Dominant Prong of the LV MS

As clearly seen in Figure 3, the MS of LV originates at the apex and bifurcates towards the aortic and mitral valves. The landmark of our choice lies at the terminal of one of these prongs. Since the aortic valve is closed during the *diastolic* phase, the distance coding of the prong terminating on this valve will be stronger (this can be clearly seen in the left prong of Figure 3). This fact is made use of to traverse and track the landmark.

A path coherent tracking framework is employed to trace the prong on the MS. Figure 4 illustrates the tracking scheme. The center, being least prone to noise from boundary perturbations, is chosen as the seed point and the tracking is extended in either direction along the first principal component. The prong is directionally propagated by evaluating its 'coherence' within an 8-connected neighborhood.

For every candidate location X_i in step $N+1$, the coherence with respect to the accumulated trajectory over n previous steps is calculated as:

$$\psi(X_{i,N+1} | trajectory_{N,n-1,...,N-(n-1),N-n}) = w_1(1-a) + w_2b$$

where, $a = \|X_{i,N+1} - trajectory_N\|^2$ is the distance to the previous point in the accumulated trajectory of the prong and $b = (\vec{v}_1 \vec{v}_2 / \|\vec{v}_1\| \|\vec{v}_2\|) - (\vec{v}_3 \vec{v}_2 / \|\vec{v}_3\| \|\vec{v}_2\|)$ is deviation in angle from the previous trajectory with the addition of the X_i (refer Figure 4). The weights w_1 and w_2 that sum up to 1 are suitably adjusted to propagate the dominant prong. All the candidate locations on MS are evaluated for their coherence and their weighted average is then assigned as the new outgrowth of the prong. This procedure is repeated until the prong breaches the surface of the shape; the breach point is taken as the landmark for the final refinement to maximize the in-plane inter-subject LV consistency.

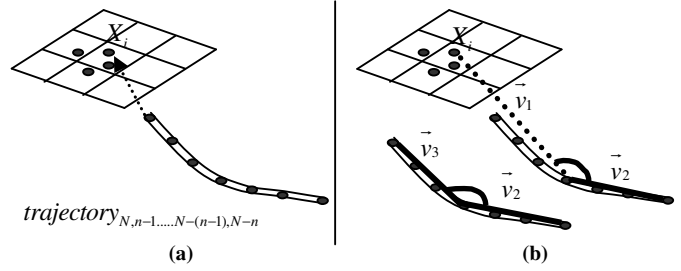


Figure 4. Path Coherence Tracking: Four different candidates in an 8-connected neighborhood along the principal Eigen vector evaluated for (a) Distance to previous trajectory (b) Angular agreement with previous trajectory. The weighted average of candidates is chosen as the outgrowth of the dominant prong.

2.3.2.3 Final in-plane alignment

The plane formed by the principal eigen vector of the LV and the terminal of the MS prong tracked as described in the previous section is rotated about the "common axis" described in section 2.3.1 until it aligns with the XZ plane as shown in Figure 5. This procedure ensures that all the datasets have their LV aligned to the common x-axes and the aortic valve-axis plane is aligned to the XZ planes thereby ensuring an "attitudinally consistent orientation" that captures the physioanatomic and pathologic variations of the LV morphology

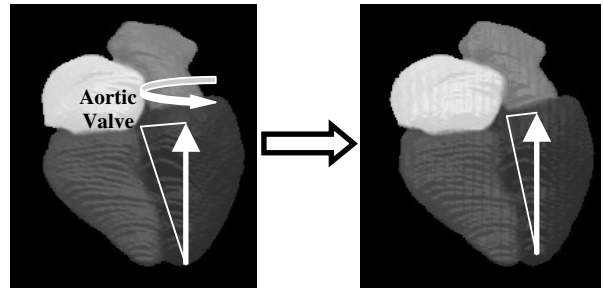


Figure 5: In-plane alignment of pose using the plane formed by LV principal axis and the aortic valve.

3. RESULTS

The results of the individual steps of the proposed approach have already been shown in the respective sections. To assess the efficacy of cascading all the steps, two groups of hearts with disparate LV volumes were considered. The basic premise for this consideration is that different stroke volumes at the same interval of the cardiac phase indicates the physioanatomic variations that correlate with normal or pathological state. First group consisted of 19 LV shape models with a mean volume of 281.9 ± 17.2 ml; the second group consisted of 16 models with a mean volume of 150.6 ± 5.8 ml. Pair wise similarity between the models within the two groups was computed both in the native and aligned space. Dice Similarity Coefficient (DSC) was used as the

similarity metric. The glyphs in Figure 6 showing all the pair wise DSCs clearly reveal the strong similarity in the "attitudinally consistent orientation" space. The graph in Figure 7 shows the mean DSCs before and after alignment of the two groups; the statistics agrees with the visual glyph shown in Figure 6.

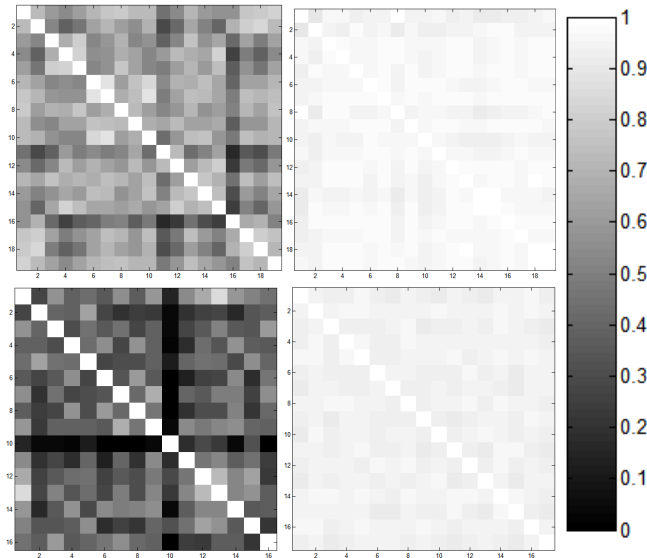


Figure 6. Pair wise DSC between the LV shape models of group 1 (top row) and group 2 (bottom row). The pair wise DSCs are shaded as shown in the colorbar; white shades indicate higher similarity. The DSCs shown in the left and right column correspond respectively to those before and after the independent alignment to the "attitudinally consistent orientation".

4. CONCLUSIONS

In brain mapping the Talairach space is often used as the unifying co-ordinate system to consistently align inter and intra- subject brain datasets. However, such a unified space does not exist for cardiac datasets. This paper made the first stride in this direction. By exploiting the clinically accepted "consistent attitudinal orientation" and incorporating the salient features of the cardiac architecture, the proposed method **independently** reorients the LV shape model into a common space so as to maximize the shape similarity and capture the physioanatomic and pathologic variations of the LV morphology. While the computational complexity is not addressed here, it should be convincing that given the simplicity of individual steps the turn-around time for alignment is orders of magnitude faster than existing techniques that simultaneously operate on all the datasets. The proposed approach might have profound implications in creating pathology specific cardiac atlases and potentially contribute to improved understanding and treatment of cardiac diseases.

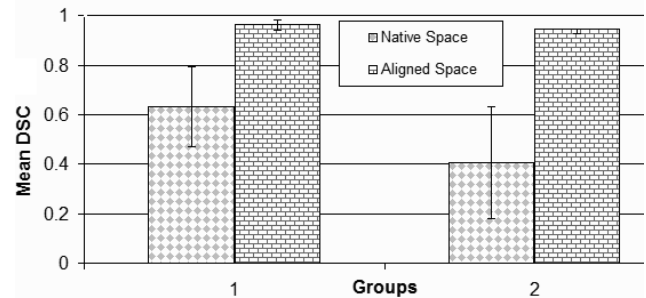


Figure 7. Mean DSCs before and after alignment for the two groups of LV shape models.

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